WE CLAIM:

1. A method for prenatal diagnosis of chromosomal abnormality in a predetermined DNA region comprising the steps of:

a) obtaining a plasma sample from a pregnant female;
b) digesting DNA from said plasma sample with an enzyme that selectively and substantially completely digests the maternal DNA to obtain a DNA sample enriched for fetal DNA regions; and
c) determining the paternal or maternal allele frequency using polymorphic markers adjacent to or within the fetal DNA regions in the sample of step (b),

wherein a difference in allele frequency from other than 50% of paternal and 50% of maternal allele as compared to a normal control, which does not comprise a chromosomal abnormality is indicative of a chromosomal abnormality.

2. The method of claim 1, wherein the DNA is isolated from the plasma sample before it is digested.

3. The method of claim 1, wherein comparing the paternal or maternal allele frequency of step (c) is performed against at least one internal control located in a chromosome, duplication or deletion of which is not a target of diagnosis, and wherein both maternal and paternal alleles are present in equal amount, wherein deviation of the ratio from the internal control indicates presence of chromosomal abnormality.

4. The method of claim 1 further comprising a DNA amplification step performed after step (a) and before step (c).

5. The method of claim 1, wherein said enzyme of step (b) is a methyl-sensitive enzyme.

6. The method of claim 5, wherein said methyl-sensitive enzyme digests only at DNA recognition sites that are unmethylated and wherein the maternal or paternal allele frequency is determined using polymorphic markers adjacent to or within methylated fetal DNA regions.

7. The method of claim 3, wherein said methyl-sensitive enzyme digests only at DNA recognition sites that are methylated, and wherein the maternal or paternal allele frequency is determined using polymorphic markers adjacent to or within unmethylated fetal DNA regions.

8. A method for prenatal diagnosis of chromosomal abnormality comprising the steps of:

a) obtaining a plasma sample from a pregnant female;
b) digesting nucleic acids present in said plasma sample with a methyl-sensitive enzyme that digests only unmethylated DNA;
c) optionally isolating undigested nucleic acid from step (b);
d) amplifying the undigested nucleic acid from step (b) or (c) while using a nucleic acid methylase to methylate nascent hemi-methylated nucleic acid;
e) digesting amplified nucleic acid of step (d) with a methyl-sensitive enzyme that digests only unmethylated nucleic acid; and
f) determining the paternal or maternal allele frequency using polymorphic markers adjacent to or within unmethylated fetal nucleic acid regions,

wherein a difference in allele frequency other than 50% of maternal and 50% of paternal is indicative of a chromosomal abnormality.

9. The method of claim 8, wherein the comparing of the paternal or maternal allele frequency of step (f) is performed against to a control nucleic acid sample, wherein a difference of other than the ratio in the control sample is indicative of a chromosomal abnormality.

10. The method of claim 8, wherein the nucleic acid is DNA.

11. The method of claim 8, wherein the nucleic acid is isolated from the plasma sample before it is digested.

12. The method of claim 1 or 8, wherein the chromosomal abnormality is DNA duplication.

13. The method of claim 1 or 8, wherein the chromosomal abnormality is a DNA deletion.

14. The method of claim 1 or 8, wherein the chromosomal abnormality is aneuploidy.

15. The method of claim 14, wherein said aneuploidy is selected from the group consisting of trisomy 21, trisomy 18, and trisomy 13.

16. A method of diagnosing fetal chromosomal abnormality comprising the steps of:

a) obtaining a plasma sample from a pregnant female;

b) selectively treating said plasma sample to enrich the sample for at least one fetal nucleic acid region;

c) determining the paternal or maternal allele frequency using at least one polymorphic marker adjacent to or within the at least one fetal nucleic acid region in the sample of step (b); and

d) comparing the paternal or maternal allele frequency of step (c) to a control DNA sample, wherein a difference in allele frequency from other than 50% of paternal and 50% of maternal allele is indicative of a chromosomal abnormality.

17. A method of diagnosing fetal chromosomal abnormality comprising the steps of:

a) obtaining a plasma sample from a pregnant female;

b) selectively treating said plasma sample to enrich the sample for at least one fetal nucleic acid region;

c) determining the paternal or maternal allele frequency using at least one polymorphic marker adjacent to or within the at least one fetal nucleic acid region in the sample of step (b); and

d) comparing the paternal or maternal allele frequency of step (c) to a control DNA sample wherein the maternal and paternal alleles are present in predetermined amounts, wherein a difference in allele frequency from other than 50% of paternal and 50% of maternal allele as compared to the control is indicative of a chromosomal abnormality.

18. A kit for prenatal diagnosis of chromosomal abnormalities comprising a methylation-sensitive enzyme, at least one pair of nucleic acid amplification primers capable of annealing and thus amplifying regions flanking sites that contain at least one polymorphic locus within differentially methylated regions in fetal and maternal DNA present in maternal plasma, at least one primer or probe to allow detection of alleles in the at least one polymorphic locus, and an instruction manual instructing the user to perform the steps of taking a plasma sample from a pregnant female, selectively digesting the nucleic acids present in said plasma sample with the methylation-sensitive enzyme to enrich the fetal nucleic acids in the sample, performing nucleic acid amplification using the amplification primers and detecting the alleles present in the sample enriched for the fetal nucleic acids, and interpreting the results so that if the ratio of two different alleles in the locus deviates from a control wherein the alleles are present in equal amounts, the fetus is affected with a chromosomal abnormality.

19. The kit of claim 18, further comprising a control nucleic acid panel, wherein the controls comprise nucleic acids isolated from females pregnant with fetuses carrying known chromosomal abnormalities and females pregnant with fetuses without chromosomal abnormalities.

20. The kit of claim 19, further comprising an internal control of at least one pair of amplification primers and a detection primer or probe, wherein the primers and/or probe are selected from a nucleic acid region that is differentially methylated in fetal and maternal DNA present in maternal plasma, but that occur in chromosomes, wherein duplication or deletion is rare, so as to provide an internal control.

21. The kit of claim 19, wherein the prenatal diagnosis is for chromosome 13, 18 or 21 duplications and the internal control is located in any other autosome than 13, 18, or 21.